

OIPE

## RAW SEQUENCE LISTING

DATE: 06/28/2001

PATENT APPLICATION: US/09/880,371

TIME: 14:43:02

Input Set : A:\E911.app

Output Set: N:\CRF3\06282001\I880371.raw

3 <110> APPLICANT: Wei, Zhong-Min  
 4 DeRocher, Jay  
 6 <120> TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC  
 7 PLANTS  
 9 <130> FILE REFERENCE: 21829/91  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/880,371  
 C--> 12 <141> CURRENT FILING DATE: 2001-06-13  
 14 <150> PRIOR APPLICATION NUMBER: 60/211,585  
 15 <151> PRIOR FILING DATE: 2000-06-15  
 17 <160> NUMBER OF SEQ ID NOS: 16  
 19 <170> SOFTWARE: PatentIn Ver. 2.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 338  
 23 <212> TYPE: PRT  
 24 <213> ORGANISM: Erwinia chrysanthemi  
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 31 20 25 30  
 33 Leu Gly Ser Ser Val Asp Lys Leu Ser Ser Thr Ile Asp Lys Leu Thr  
 34 35 40 45  
 36 Ser Ala Leu Thr Ser Met Met Phe Gly Gly Ala Leu Ala Gln Gly Leu  
 37 50 55 60  
 39 Gly Ala Ser Ser Lys Gly Leu Gly Met Ser Asn Gln Leu Gly Gln Ser  
 40 65 70 75 80  
 42 Phe Gly Asn Gly Ala Gln Gly Ala Ser Asn Leu Leu Ser Val Pro Lys  
 43 85 90 95  
 45 Ser Gly Gly Asp Ala Leu Ser Lys Met Phe Asp Lys Ala Leu Asp Asp  
 46 100 105 110  
 48 Leu Leu Gly His Asp Thr Val Thr Lys Leu Thr Asn Gln Ser Asn Gln  
 49 115 120 125  
 51 Leu Ala Asn Ser Met Leu Asn Ala Ser Gln Met Thr Gln Gly Asn Met  
 52 130 135 140  
 54 Asn Ala Phe Gly Ser Gly Val Asn Asn Ala Leu Ser Ser Ile Leu Gly  
 55 145 150 155 160  
 57 Asn Gly Leu Gly Gln Ser Met Ser Gly Phe Ser Gln Pro Ser Leu Gly  
 58 165 170 175  
 60 Ala Gly Gly Leu Gln Gly Leu Ser Gly Ala Gly Ala Phe Asn Gln Leu  
 61 180 185 190  
 63 Gly Asn Ala Ile Gly Met Gly Val Gly Gln Asn Ala Ala Leu Ser Ala  
 64 195 200 205  
 66 Leu Ser Asn Val Ser Thr His Val Asp Gly Asn Asn Arg His Phe Val  
 67 210 215 220  
 69 Asp Lys Glu Asp Arg Gly Met Ala Lys Glu Ile Gly Gln Phe Met Asp  
 70 225 230 235 240  
 72 Gln Tyr Pro Glu Ile Phe Gly Lys Pro Glu Tyr Gln Lys Asp Gly Trp

ENTERED

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73          245          250          255
75 Ser Ser Pro Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser Lys
76          260          265          270
78 Pro Asp Asp Asp Gly Met Thr Gly Ala Ser Met Asp Lys Phe Arg Gln
79          275          280          285
81 Ala Met Gly Met Ile Lys Ser Ala Val Ala Gly Asp Thr Gly Asn Thr
82          290          295          300
84 Asn Leu Asn Leu Arg Gly Ala Gly Gly Ala Ser Leu Gly Ile Asp Ala
85 305          310          315          320
87 Ala Val Val Gly Asp Lys Ile Ala Asn Met Ser Leu Gly Lys Leu Ala
88          325          330          335
90 Asn Ala
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95 <211> LENGTH: 2141
96 <212> TYPE: DNA
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103 cagcaatatac ccggcatggt gccgacgctg ctgcctcgtc gttatcagca ggccgagag 240
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106 acgttgccgt cgtatccat agcaccgacg gcgcgtccgc agacagggaa cggacgcgcc 420
107 cgatcattaa gataaaggcg gcttttttta ttgcaaaacg gtaacggtga ggaaccgttt 480
108 caccgtcggc gtcactcagt aacaagtatc catcatgatg cctacatcgg gatcggcgctg 540
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110 aattacgatac aaagcgcaca tggcggtga tttggcgctc tccggtctgg ggctgggtgc 660
111 tcagggactg aaaggactga attccgcggc ttcacgctg ggttccagcg tggataaact 720
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113 ggccgagggg ctgggcgccca gctcgaaggg gctggggatg agcaatcaac tgggccagtc 840
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115 tgcgttgctc aaaatgtttg ataaagcgt ggacgatctg ctgggtcatg acaccgtgac 960
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117 ccagggtaat atgaatgcgt tcggcagcgg tgtgaacaac gcaactgtct ccattctcgg 1080
118 caacggtctc ggccagtcga tgagtgcct ctctcagcct tctctggggg caggcggtt 1140
119 gcagggcctg agcggcgcg gtgcattcaa ccagttgggt aatgccatcg gcatggcgct 1200
120 ggggcagaat gctgcgtga gtgcgttgag taacgtcagc acccacgtag acggtaaaca 1260
121 ccgccacttt gtagataaag aagatcgcg catggcgaaa gagatcggcc agtttatgga 1320
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126 ggctgtcgtc ggcgataaaa tagccaacat gtcgtgggt aagctggcca acgcctgata 1620
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130 gtcgctcaga ttgcgcggct gatggggaac gccgggtgga atatagagaa actcgccggc 1860
131 cagatggaga cagctctgct ataaatctgt gccgtaacgt gtttctatcc gcccttttag 1920

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132 cagatagatt gcggtttcgt aatcaacatg gtaatgcggt tccgcctgtg cgccggccgg 1980
133 gatcaccaca atattcatag aaagctgtct tgcacctacc gtatcgcggg agataccgac 2040
134 aaaatagggc agtttttgcg tggatccgt ggggtgttcc ggcctgacaa tcttgagttg 2100
135 gttcgtcatc atctttctcc atctgggcga cctgatcggt t 2141
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139 <211> LENGTH: 403
140 <212> TYPE: PRT
141 <213> ORGANISM: Erwinia amylovora
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147 Ile Gly Gly Ala Gly Gly Asn Asn Gly Leu Leu Gly Thr Ser Arg Gln
148 20 25 30
150 Asn Ala Gly Leu Gly Gly Asn Ser Ala Leu Gly Leu Gly Gly Asn
151 35 40 45
153 Gln Asn Asp Thr Val Asn Gln Leu Ala Gly Leu Leu Thr Gly Met Met
154 50 55 60
156 Met Met Met Ser Met Met Gly Gly Gly Gly Leu Met Gly Gly Gly Leu
157 65 70 75 80
159 Gly Gly Gly Leu Gly Asn Gly Leu Gly Gly Ser Gly Gly Leu Gly Glu
160 85 90 95
162 Gly Leu Ser Asn Ala Leu Asn Asp Met Leu Gly Gly Ser Leu Asn Thr
163 100 105 110
165 Leu Gly Ser Lys Gly Gly Asn Asn Thr Thr Ser Thr Thr Asn Ser Pro
166 115 120 125
168 Leu Asp Gln Ala Leu Gly Ile Asn Ser Thr Ser Gln Asn Asp Asp Ser
169 130 135 140
171 Thr Ser Gly Thr Asp Ser Thr Ser Asp Ser Ser Asp Pro Met Gln Gln
172 145 150 155 160
174 Leu Leu Lys Met Phe Ser Glu Ile Met Gln Ser Leu Phe Gly Asp Gly
175 165 170 175
177 Gln Asp Gly Thr Gln Gly Ser Ser Ser Gly Gly Lys Gln Pro Thr Glu
178 180 185 190
180 Gly Glu Gln Asn Ala Tyr Lys Lys Gly Val Thr Asp Ala Leu Ser Gly
181 195 200 205
183 Leu Met Gly Asn Gly Leu Ser Gln Leu Leu Gly Asn Gly Gly Leu Gly
184 210 215 220
186 Gly Gly Gln Gly Gly Asn Ala Gly Thr Gly Leu Asp Gly Ser Ser Leu
187 225 230 235 240
189 Gly Gly Lys Gly Leu Gln Asn Leu Ser Gly Pro Val Asp Tyr Gln Gln
190 245 250 255
192 Leu Gly Asn Ala Val Gly Thr Gly Ile Gly Met Lys Ala Gly Ile Gln
193 260 265 270
195 Ala Leu Asn Asp Ile Gly Thr His Arg His Ser Ser Thr Arg Ser Phe
196 275 280 285
198 Val Asn Lys Gly Asp Arg Ala Met Ala Lys Glu Ile Gly Gln Phe Met
199 290 295 300
201 Asp Gln Tyr Pro Glu Val Phe Gly Lys Pro Gln Tyr Gln Lys Gly Pro
202 305 310 315 320

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204 Gly Gln Glu Val Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser
205           325           330           335
207 Lys Pro Asp Asp Asp Gly Met Thr Pro Ala Ser Met Glu Gln Phe Asn
208           340           345           350
210 Lys Ala Lys Gly Met Ile Lys Arg Pro Met Ala Gly Asp Thr Gly Asn
211           355           360           365
213 Gly Asn Leu Gln Ala Arg Gly Ala Gly Gly Ser Ser Leu Gly Ile Asp
214           370           375           380
216 Ala Met Met Ala Gly Asp Ala Ile Asn Asn Met Ala Leu Gly Lys Leu
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223 <210> SEQ ID NO: 4
224 <211> LENGTH: 1288
225 <212> TYPE: DNA
226 <213> ORGANISM: Erwinia amylovora
228 <400> SEQUENCE: 4
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230 gaggaatacy ttatgagtct gaatacaagt gggctgggag cgtcaacgat gcaaatttct 120
231 atcggcggtg cgggcggaaa taacgggttg ctgggtacca gtcgccagaa tgctgggttg 180
232 ggtggcaatt ctgcactggg gctgggcggc ggtaatcaaa atgataccgt caatcagctg 240
233 gctggcttac tcaccggcat gatgatgat atgagcatga tgggcggttg tgggctgatg 300
234 ggcggtggct taggcggttg cttaggtaat ggcttgggtg gctcagggtg cctgggcgaa 360
235 ggactgtcga acgcgctgaa cgatatgtta ggcggttcgc tgaacacgct gggctcgaaa 420
236 ggcggcaaca ataccacttc aacaacaaat tccccgctgg accaggcgct gggatttaac 480
237 tcaacgtccc aaaacgacga ttccacctcc ggcacagatt ccacctcaga ctccagcgac 540
238 cggatgcagc agctgctgaa gatgttcagc gagataatgc aaagcctgtt tggatgatgg 600
239 caagatggca cccagggcag ttctctctgg ggcaagcagc cgaccgaagg cgagcagaac 660
240 gcctataaaa aaggagtcac tgatgcgctg tcgggcctga tgggtaatgg tctgagccag 720
241 ctctctggca acgggggact gggaggtggt cagggcggtg atgctggcac gggctttgac 780
242 ggttcgctgc tgggcggcaa agggctgcaa aacctgagcg ggcggttgga ctaccagcag 840
243 ttaggtaacg ccgtgggtac cggtatcggg atgaaagcgg gcattcaggc gctgaatgat 900
244 atcggtaacg acaggcacag ttcaaccctg tctttcgtca ataaaggcga tcgggcgatg 960
245 gcgaaggaaa tcggtcagtt catggaccag tatcctgagg tgtttggcaa gccgcagtac 1020
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247 aagccagatg acgacggaat gacaccagcc agtatggagc agttcaacaa agccaagggc 1140
248 atgatcaaaa ggcccatggc gggtgatacc ggcaacggca acctgcaggc acgcggtgcc 1200
249 ggtgggttctt cgctgggtat tgatgccatg atggccggtg atgccattaa caatatggca 1260
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253 <210> SEQ ID NO: 5
254 <211> LENGTH: 447
255 <212> TYPE: PRT
256 <213> ORGANISM: Erwinia amylovora
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262 Phe Gln Ser Gly Gly Asp Asn Gly Leu Gly Gly His Asn Ala Asn Ser
263           20           25           30
265 Ala Leu Gly Gln Gln Pro Ile Asp Arg Gln Thr Ile Glu Gln Met Ala
266           35           40           45

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268 Gln Leu Leu Ala Glu Leu Leu Lys Ser Leu Leu Ser Pro Gln Ser Gly
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271 Asn Ala Ala Thr Gly Ala Gly Gly Asn Asp Gln Thr Thr Gly Val Gly
272 65                      70                      75                      80
274 Asn Ala Gly Gly Leu Asn Gly Arg Lys Gly Thr Ala Gly Thr Thr Pro
275                      85                      90                      95
277 Gln Ser Asp Ser Gln Asn Met Leu Ser Glu Met Gly Asn Asn Gly Leu
278                      100                      105                      110
280 Asp Gln Ala Ile Thr Pro Asp Gly Gln Gly Gly Gly Gln Ile Gly Asp
281                      115                      120                      125
283 Asn Pro Leu Leu Lys Ala Met Leu Lys Leu Ile Ala Arg Met Met Asp
284                      130                      135                      140
286 Gly Gln Ser Asp Gln Phe Gly Gln Pro Gly Thr Gly Asn Asn Ser Ala
287 145                      150                      155                      160
289 Ser Ser Gly Thr Ser Ser Ser Gly Gly Ser Pro Phe Asn Asp Leu Ser
290                      165                      170                      175
292 Gly Gly Lys Ala Pro Ser Gly Asn Ser Pro Ser Gly Asn Tyr Ser Pro
293                      180                      185                      190
295 Val Ser Thr Phe Ser Pro Pro Ser Thr Pro Thr Ser Pro Thr Ser Pro
296                      195                      200                      205
298 Leu Asp Phe Pro Ser Ser Pro Thr Lys Ala Ala Gly Gly Ser Thr Pro
299                      210                      215                      220
301 Val Thr Asp His Pro Asp Pro Val Gly Ser Ala Gly Ile Gly Ala Gly
302 225                      230                      235                      240
304 Asn Ser Val Ala Phe Thr Ser Ala Gly Ala Asn Gln Thr Val Leu His
305                      245                      250                      255
307 Asp Thr Ile Thr Val Lys Ala Gly Gln Val Phe Asp Gly Lys Gly Gln
308                      260                      265                      270
310 Thr Phe Thr Ala Gly Ser Glu Leu Gly Asp Gly Gly Gln Ser Glu Asn
311                      275                      280                      285
313 Gln Lys Pro Leu Phe Ile Leu Glu Asp Gly Ala Ser Leu Lys Asn Val
314                      290                      295                      300
316 Thr Met Gly Asp Asp Gly Ala Asp Gly Ile His Leu Tyr Gly Asp Ala
317 305                      310                      315                      320
319 Lys Ile Asp Asn Leu His Val Thr Asn Val Gly Glu Asp Ala Ile Thr
320                      325                      330                      335
322 Val Lys Pro Asn Ser Ala Gly Lys Lys Ser His Val Glu Ile Thr Asn
323                      340                      345                      350
325 Ser Ser Phe Glu His Ala Ser Asp Lys Ile Leu Gln Leu Asn Ala Asp
326                      355                      360                      365
328 Thr Asn Leu Ser Val Asp Asn Val Lys Ala Lys Asp Phe Gly Thr Phe
329                      370                      375                      380
331 Val Arg Thr Asn Gly Gly Gln Gln Gly Asn Trp Asp Leu Asn Leu Ser
332 385                      390                      395                      400
334 His Ile Ser Ala Glu Asp Gly Lys Phe Ser Phe Val Lys Ser Asp Ser
335                      405                      410                      415
337 Glu Gly Leu Asn Val Asn Thr Ser Asp Ile Ser Leu Gly Asp Val Glu
338                      420                      425                      430
340 Asn His Tyr Lys Val Pro Met Ser Ala Asn Leu Lys Val Ala Glu

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/880,371

DATE: 06/28/2001

TIME: 14:43:03

Input Set : A:\E911.app

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date